

SEQUENCE LISTING

<110> WANG, XIAODONG  
LIU, XUESONG

<120> DNA FRAGMENTATION FACTOR INVOLVED IN APOPTOSIS

<130> UTSD:546USD1

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<141> 2000-12-22

<150> 09/061,702

<151> 1998-04-16

<160> 21

<170> PatentIn Ver. 2.1

<210> 1

<211> 2839

<212> DNA

<213> Homo sapiens

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2025 RELEASE UNDER E.O. 14176

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<212> PRT

<213> Homo sapiens

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20                          25                          30

Gly Cys Leu Arg Phe Gln Leu Pro Glu Arg Gly Ser Arg Leu Cys Leu

35                          40                          45

Tyr Glu Asp Gly Thr Glu Leu Thr Glu Asp Tyr Phe Pro Ser Val Pro

50                    55                    60

Asp Asn Ala Glu Leu Val Leu Leu Thr Leu Gly Gln Ala Trp Gln Gly

65                    70                    75                    80

DRAFT

Tyr Val Ser Asp Ile Arg Arg Phe Leu Ser Ala Phe His Glu Pro Gln  
85 90 95

Val Gly Leu Ile Gln Ala Ala Gln Gln Leu Leu Cys Asp Glu Gln Ala  
100 105 110

Pro Gln Arg Gln Arg Leu Leu Ala Asp Leu Leu His Asn Val Ser Gln  
115 120 125

Asn Ile Ala Ala Glu Thr Arg Ala Glu Asp Pro Pro Trp Phe Glu Gly  
130 135 140

Leu Glu Ser Arg Phe Gln Ser Lys Ser Gly Tyr Leu Arg Tyr Ser Cys  
145 150 155 160

Glu Ser Arg Ile Arg Ser Tyr Leu Arg Glu Val Ser Ser Tyr Pro Ser  
165 170 175

Thr Val Gly Ala Glu Ala Gln Glu Glu Phe Leu Arg Val Leu Gly Ser  
180 185 190

Met Cys Gln Arg Leu Arg Ser Met Gln Tyr Asn Gly Ser Tyr Phe Asp  
195 200 205

Arg Gly Ala Lys Gly Gly Ser Arg Leu Cys Thr Pro Glu Gly Trp Phe  
210 215 220

Ser Cys Gln Gly Pro Phe Asp Met Asp Ser Cys Leu Ser Arg His Ser  
225 230 235 240

Ile Asn Pro Tyr Ser Asn Arg Glu Ser Arg Ile Leu Phe Ser Thr Trp  
245 250 255

Asn Leu Asp His Ile Ile Glu Lys Lys Arg Thr Ile Ile Pro Thr Leu  
260 265 270

Val Glu Ala Ile Lys Glu Gln Asp Gly Arg Glu Val Asp Trp Glu Tyr  
275 280 285

Phe Tyr Gly Leu Leu Phe Thr Ser Glu Asn Leu Lys Leu Val His Ile  
290 295 300

Val Cys His Lys Lys Thr Thr His Lys Leu Asn Cys Asp Pro Ser Arg  
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Arg Gln

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<213> Homo sapiens

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Met Glu  
1

gtg acc ggg gac gcc ggg gta cca gaa tct ggc gag atc cg<sup>g</sup> act cta 166  
Val Thr Gly Asp Ala Gly Val Pro Glu Ser Gly Glu Ile Arg Thr Leu  
5 10 15

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Lys Pro Cys Leu Leu Arg Arg Asn Tyr Ser Arg Glu Gln His Gly Val
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Ala Ala Ser Cys Leu Glu Asp Leu Arg Ser Lys Ala Cys Asp Ile Leu  
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gcc att gat aag tcc ctg aca cca gtc acc ctt gtc ctg gca gag gat 310  
Ala Ile Asp Lys Ser Leu Thr Pro Val Thr Leu Val Leu Ala Glu Asp  
55 60 65

ggc acc ata gtg gat gat gac gat tac ttt ctg tgt cta cct tcc aat 358  
Gly Thr Ile Val Asp Asp Asp Asp Tyr Phe Leu Cys Leu Pro Ser Asn  
70 75 80

act aag ttt gtg gca ttg gct agt aat gag aaa tgg gca tac aac aat 406  
Thr Lys Phe Val Ala Leu Ala Ser Asn Glu Lys Trp Ala Tyr Asn Asn  
85 90 95

tca gat gga ggt aca gct tgg att tcc caa gag tcc ttt gat gta gat 454  
Ser Asp Gly Gly Thr Ala Trp Ile Ser Gln Glu Ser Phe Asp Val Asp  
100 105 110

Gly Ser Val Leu Ile Asp Glu Lys Cys Pro Ala Val

gaa aca gac agc ggg gca ggg ttg aag tgg aat gtg gcc agg gag			502
Glu Thr Asp Ser Gly Ala Gly Leu Lys Trp Lys Asn Val Ala Arg Glu			
115	120	125	130
ctg aaa gaa gat ctg tcc agc atc atc ctc cta tca gag gag gac ctc			550
Leu Lys Glu Asp Leu Ser Ser Ile Ile Leu Leu Ser Glu Glu Asp Leu			
135	140	145	
cag atg ctt gtt gac gct ccc tgc tca gac ctg gct cag gaa cta cgt			598
Gln Met Leu Val Asp Ala Pro Cys Ser Asp Leu Ala Gln Glu Leu Arg			
150	155	160	
cag agt tgt gcc acc gtc cag cgg ctg cag cac aca ctc caa cag gtg			646
Gln Ser Cys Ala Thr Val Gln Arg Leu Gln His Thr Leu Gln Gln Val			
165	170	175	
ctt gac caa aga gag gaa gtg cgt cag tcc aag cag ctc ctg cag ctg			694
Leu Asp Gln Arg Glu Glu Val Arg Gln Ser Lys Gln Leu Leu Gln Leu			
180	185	190	
tac ctc cag gct ttg gag aaa gag ggc agc ctc ttg tca aag cag gaa			742
Tyr Leu Gln Ala Leu Glu Lys Glu Gly Ser Leu Leu Ser Lys Gln Glu			
195	200	205	210
gag tcc aaa gct gcc ttt ggt gag gag gtg gat gca gta gac acg ggt			790
Glu Ser Lys Ala Ala Phe Gly Glu Glu Val Asp Ala Val Asp Thr Gly			
215	220	225	
atg agc aga gag acc tcc tcg gac gtt gcg ctg gcg agc cac atc ctt			838
Met Ser Arg Glu Thr Ser Ser Asp Val Ala Leu Ala Ser His Ile Leu			
230	235	240	
act gca ctg agg gag aag cag gct cca gag ctg agc tta tct agt cag			886
Thr Ala Leu Arg Glu Lys Gln Ala Pro Glu Leu Ser Leu Ser Ser Gln			
245	250	255	
gat ttg gag ttg gtt acc aag gaa gac ccc aaa gca ctg gct gtt gcc			934
Asp Leu Glu Leu Val Thr Lys Glu Asp Pro Lys Ala Leu Ala Val Ala			
260	265	270	
ttg aac tgg gac ata aag aag acg gag act gtt cag gag gcc tgt gag			982
Leu Asn Trp Asp Ile Lys Lys Thr Glu Thr Val Gln Glu Ala Cys Glu			
275	280	285	290
cgg gag ctc gcc ctg cgc ctg cag cag acg cag ttg cat tct ctc			1030
Arg Glu Leu Ala Leu Arg Leu Gln Gln Thr Gln Ser Leu His Ser Leu			
295	300	305	

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Arg Ser Ile Ser Ala Ser Lys Ala Ser Pro Pro Gly Asp Leu Gln Asn  
310 315 320

cct aag cga gcc aga cag gat ccc aca tagcagcagc gggaaagtgtg 1125  
Pro Lys Arg Ala Arg Gln Asp Pro Thr  
325 330

ccaaggaagc tctgtggcgt tttgttattt gtagacaccc tcagcctcat catttgacta 1185

cctatgtact actctacccc ctgccttaga gcaccccca gagaagctat tccaggctc 1245

aacatacgcc gttccaccaa tttttttt agccccacca gcttcaggac ttctgccaat 1305

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cctgtaatcc cagctacttg ggaggctgag gcaggagaat ggcatgaacc tgggaggcag 1605

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35 40 45

Ile Leu Ala Ile Asp Lys Ser Leu Thr Pro Val Thr Leu Val Leu Ala  
50 55 60

Glu Asp Gly Thr Ile Val Asp Asp Asp Tyr Phe Leu Cys Leu Pro

0974351-122200

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Asn Asn Ser Asp Gly Gly Thr Ala Trp Ile Ser Gln Glu Ser Phe Asp			
100	105	110	
Val Asp Glu Thr Asp Ser Gly Ala Gly Leu Lys Trp Lys Asn Val Ala			
115	120	125	
Arg Glu Leu Lys Glu Asp Leu Ser Ser Ile Ile Leu Leu Ser Glu Glu			
130	135	140	
Asp Leu Gln Met Leu Val Asp Ala Pro Cys Ser Asp Leu Ala Gln Glu			
145	150	155	160
Leu Arg Gln Ser Cys Ala Thr Val Gln Arg Leu Gln His Thr Leu Gln			
165	170	175	
Gln Val Leu Asp Gln Arg Glu Glu Val Arg Gln Ser Lys Gln Leu Leu			
180	185	190	
Gln Leu Tyr Leu Gln Ala Leu Glu Lys Glu Gly Ser Leu Leu Ser Lys			
195	200	205	
Gln Glu Glu Ser Lys Ala Ala Phe Gly Glu Glu Val Asp Ala Val Asp			
210	215	220	
Thr Gly Met Ser Arg Glu Thr Ser Ser Asp Val Ala Leu Ala Ser His			
225	230	235	240
Ile Leu Thr Ala Leu Arg Glu Lys Gln Ala Pro Glu Leu Ser Leu Ser			
245	250	255	
Ser Gln Asp Leu Glu Leu Val Thr Lys Glu Asp Pro Lys Ala Leu Ala			
260	265	270	
Val Ala Leu Asn Trp Asp Ile Lys Lys Thr Glu Thr Val Gln Glu Ala			
275	280	285	
Cys Glu Arg Glu Leu Ala Leu Arg Leu Gln Gln Thr Gln Ser Leu His			
290	295	300	
Ser Leu Arg Ser Ile Ser Ala Ser Lys Ala Ser Pro Pro Gly Asp Leu			
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325

330

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<210> 5
<211> 26
<212> DNA
<213> Artificial Sequence

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<223> N = Inosine

<220>
<221> modified_base
<222> (11)..(15)
<223> R = A or G

<220>
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<222> (18)..(24)
<223> Y = C or T

<220>
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<222> (10)
<223> W = A or T

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      Primer

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26

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<210> 6
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<212> DNA
<213> Artificial Sequence

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20

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<212> DNA
<213> Artificial Sequence

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<223> R = A or G

<220>
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<223> Y = C or T

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<213> Artificial Sequence
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<223> Y = C or T
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<223> N = A, C, G or T
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<220>
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<223> R = A or G

<220>

<221> modified\_base

<222> (15)

<223> D = G, C or A

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

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17

<210> 9

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<212> DNA

<213> Homo sapiens

<400> 9

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<210> 10

<211> 30

<212> DNA

<213> Homo sapiens

<400> 10

tgcataaga aaaccaccca caagctcaac

30

<210> 11

<211> 31

<212> DNA

<213> Homo sapiens

<400> 11

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31

<210> 12

<211> 58

<212> DNA

<213> Homo sapiens

<400> 12

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<210> 14  
<211> 52  
<212> DNA  
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<210> 20  
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<400> 20  
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1 5

<210> 21  
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<212> PRT  
<213> Mus musculus

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1 5